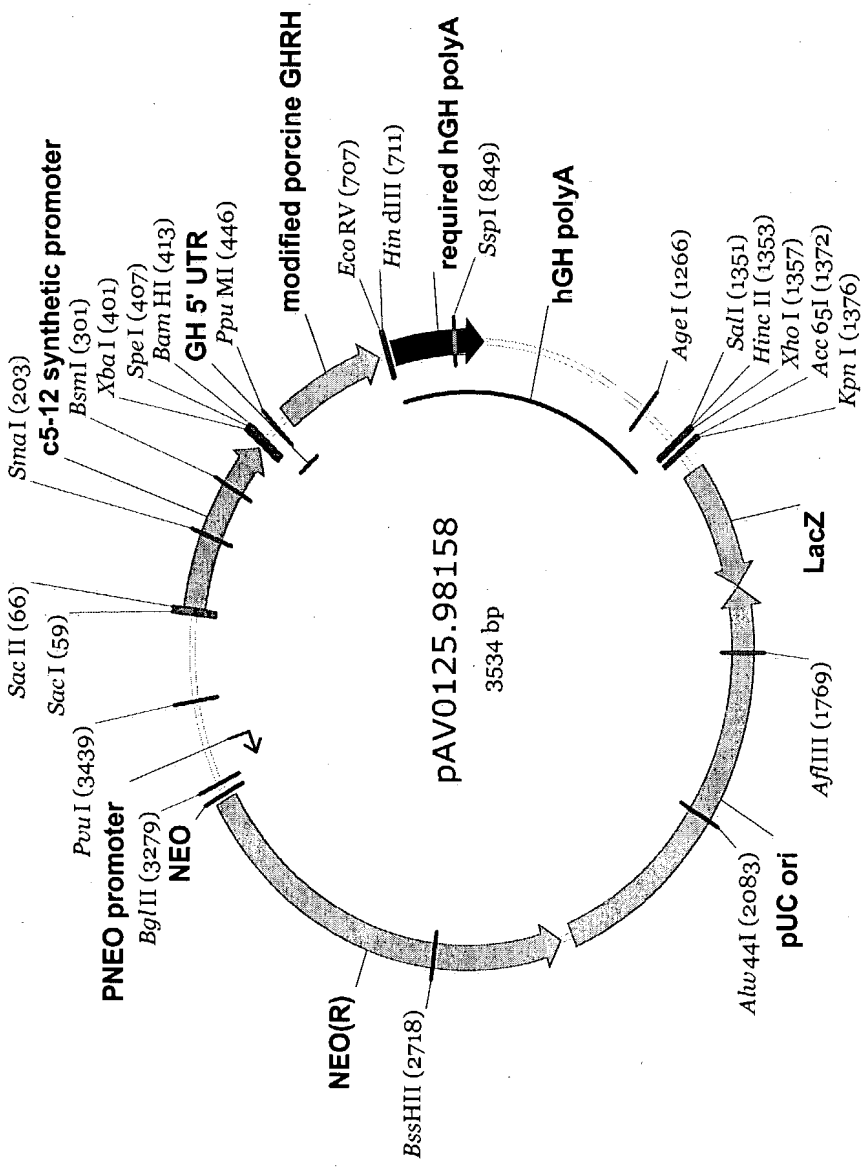
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3534 bp
modified porcine GHRH
Eco RV (707)
Hin dIII (711)
required hGH polyA
Ssp I (849)
hGH polyA
Age I (1266)
Sal I (1351)
Hinc II (1353)
Xho I (1357)
Acc 65I (1372)
Kpn I (1376)
LacZ
AflIII (1769)
Alw44I (2083)
pUC ori
BssHII (2718)
NEO(R)
Pvu I (3439)
Bgl II (3279)
NEO
PNEO promoter
Sac II (66)
Sac I (59)
Sma I (203)
c5-12 synthetic promoter
Bsm I (301)
Xba I (401)
Spe I (407)
Bam HI (413)
GH 5' UTR
Ppu MI (446)

Figure 1

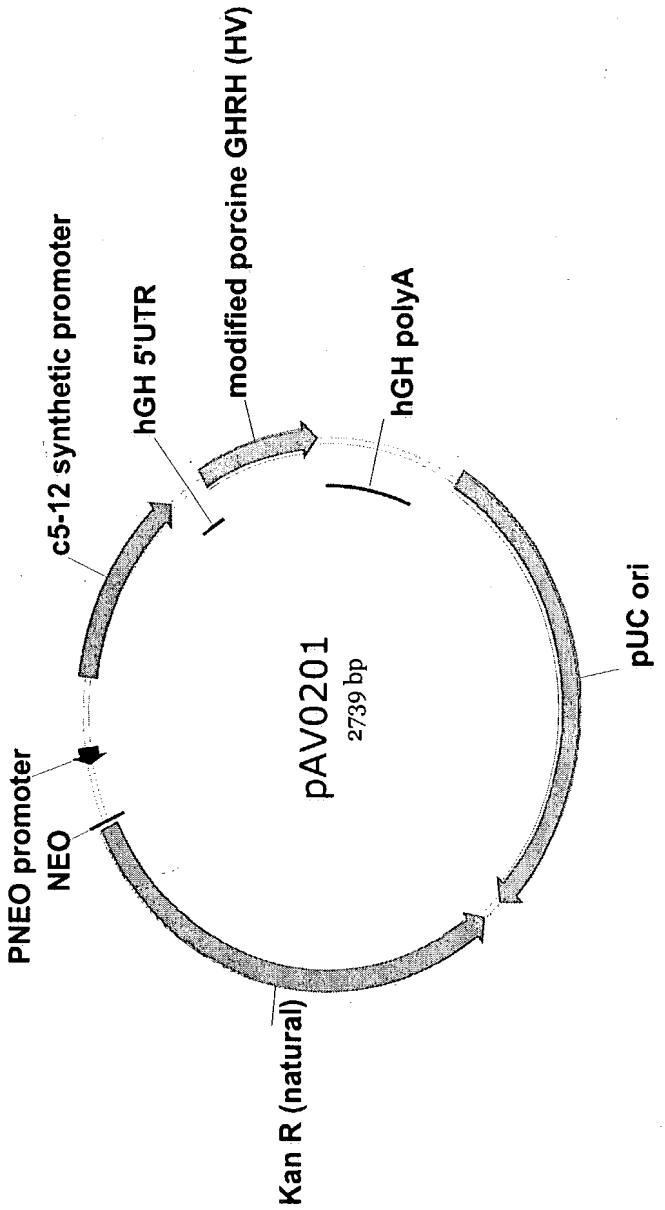
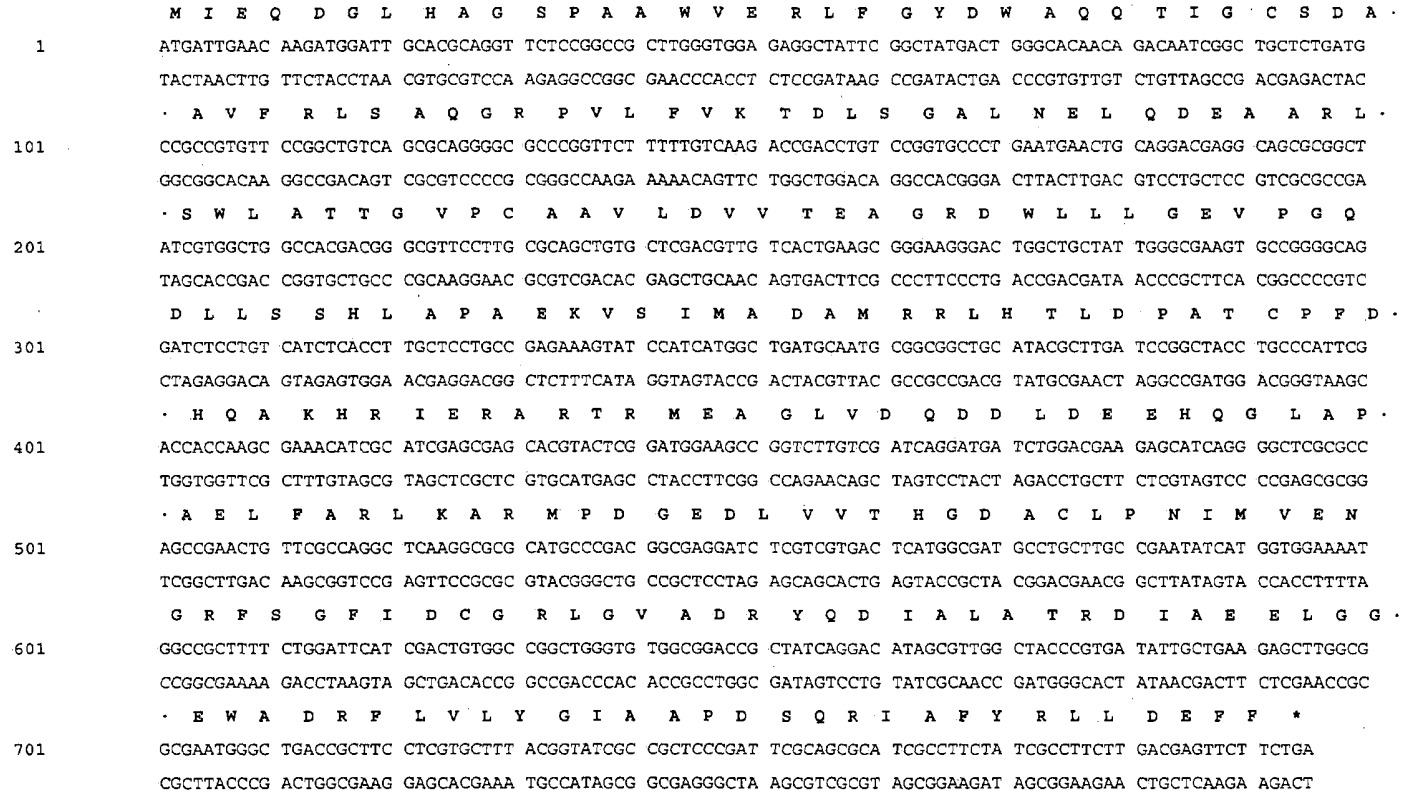

c5-12 synthetic promoter
hGH 5'UTR
modified porcine GHRH (HV)
hGH polyA
pUC ori
PNEO promoter
NEO
Kan R (natural)
pAV0201
2739 bp

Figure 2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A V F R L S A Q G R P V L F V K T D L S G A L N E L Q D E A A R L
101 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT
GGCGGCACAA GGCCGACAGT CGCGTCCCCG CGGGCCAAGA AAAACAGTTC TGGCTGGACA GGCCACGGGA CTTACTTGAC GTCCTGCTCC GTCGCGCCGA
S W L A T T G V P C A A V L D V V T E A G R D W L L L G E V P G Q
201 ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG TCACTGAAGC GGGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG
TAGCACCGAC CGGTGCTGCC CGCAAGGAAC GCGTCGACAC GAGCTGCAAC AGTGACTTCG CCCTTCCCTG ACCGACGATA ACCCGCTTCA CGGCCCCGTC
D L L S S H L A P A E K V S I M A D A M R R L H T L D P A T C P F D
301 GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCG
CTAGAGGACA GTAGAGTGGA ACGAGGACGG CTCTTTCATA GGTAGTACCG ACTACGTTAC GCCGCCGACG TATGCGAACT AGGCCGATGG ACGGGTAAGC
H Q A K H R I E R A R T R M E A G L V D Q D D L D E E H Q G L A P
401 ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC
TGGTGGTTCG CTTTGTAGCG TAGCTCGCTC GTGCATGAGC CTACCTTCGG CCAGAACAGC TAGTCCTACT AGACCTGCTT CTCGTAGTCC CCGAGCGCGG
A E L F A R L K A R M P D G E D L V V T H G D A C L P N I M V E N
501 AGCCGAACTG TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC TCGTCGTGAC TCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT
TCGGCTTGAC AAGCGGTCCG AGTTCCGCGC GTACGGGCTG CCGCTCCTAG AGCAGCACTG AGTACCGCTA CGGACGAACG GCTTATAGTA CCACCTTTTA
G R F S G F I D C G R L G V A D R Y Q D I A L A T R D I A E E L G G
601 GGCCGCTTTT CTGGATTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGGCG
CCGGCGAAAA GACCTAAGTA GCTGACACCG GCCGACCCAC ACCGCCTGGC GATAGTCCTG TATCGCAACC GATGGGCACT ATAACGACTT CTCGAACCGC
E W A D R F L V L Y G I A A P D S Q R I A F Y R L L D E F F *
701 GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGA
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Figure 3

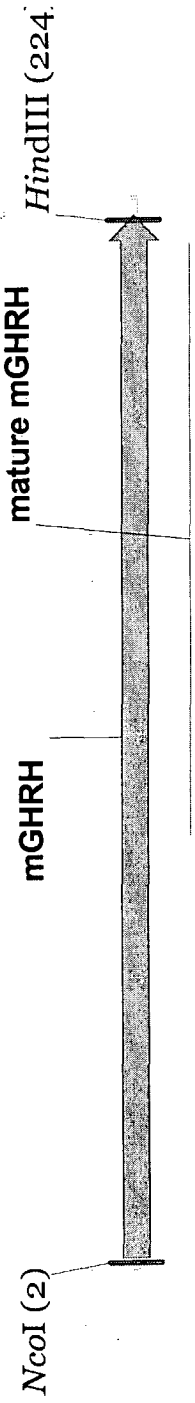

Figure 4

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  1 GCCATGGTGC TCTGGGTGCT CTTTGTGATC CTCATCCTCA CCAGCGGCAG CCACTGCAGC CTGCCTCCCA GCCCTCCCTT CAGGATGCAG AGGCACGTGG
    CGGTACCACG AGACCCACGA GAAACACTAG GAGTAGGAGT GGTCGCCGTC GGTGACGTCG GACGGAGGGT CGGGAGGGAA GTCCTACGTC TCCGTGCACC

 +3 D  A  I  F   T  T  N   Y  R  K   L  L  S  Q   L  Y  A   R  K  V   I  Q  D  I   M  N  K   Q  G  E   R  I  Q  E
101 ACGCCATCTT CACCACCAAC TACAGGAAGC TGCTGAGCCA GCTGTACGCC AGGAAGGTGA TCCAGGACAT CATGAACAAG CAGGGCGAGA GGATCCAGGA
    TGCGGTAGAA GTGGTGGTTG ATGTCCTTCG ACGACTCGGT CGACATGCGG TCCTTCCACT AGGTCCTGTA GTACTTGTTC GTCCCGCTCT CCTAGGTCCT

 +3   Q  R  A   R  L  S   &  #  A  C
201 GCAGAGGGCC AGGCTGAGCT GATAAGCTTG C
    CGTCTCCCGG TCCGACTCGA CTATTCGAAC G
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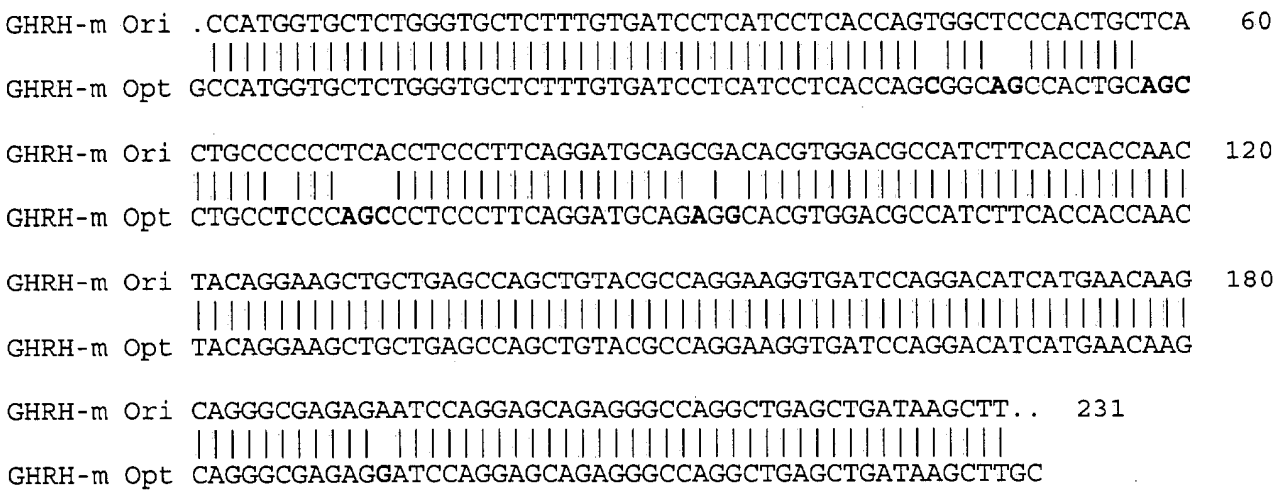
Figure 5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GHRH-m Opt GCCATGGTGCTCTGGGTGCTCTTTGTGATCCTCATCCTCACCAGCGGCAGCCACTGCAGC
GHRH-m Ori CTGCCCCCCTCACCTCCCTTCAGGATGCAGCGACACGTGGACGCCATCTTCACCACCAAC 120
GHRH-m Opt CTGCCTCCCAGCCCTCCCTTCAGGATGCAGAGGCACGTGGACGCCATCTTCACCACCAAC
GHRH-m Ori TACAGGAAGCTGCTGAGCCAGCTGTACGCCAGGAAGGTGATCCAGGACATCATGAACAAG 180
GHRH-m Opt TACAGGAAGCTGCTGAGCCAGCTGTACGCCAGGAAGGTGATCCAGGACATCATGAACAAG
GHRH-m Ori CAGGGCGAGAGAATCCAGGAGCAGAGGGCCAGGCTGAGCTGATAAGCTT.. 231
GHRH-m Opt CAGGGCGAGAGGATCCAGGAGCAGAGGGCCAGGCTGAGCTGATAAGCTTGC

Figure 6

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GHRH-M opti AMVLWVLFVILILTSGSHCSLPPSPPFRMQRHVDAIFTTNYRKLLSQLYARKVIQDIMNK

GHRH-M Ori QGERIQEQRARLSA.   75
           ||||||||||||||
GHRH-M opti QGERIQEQRARLSAC
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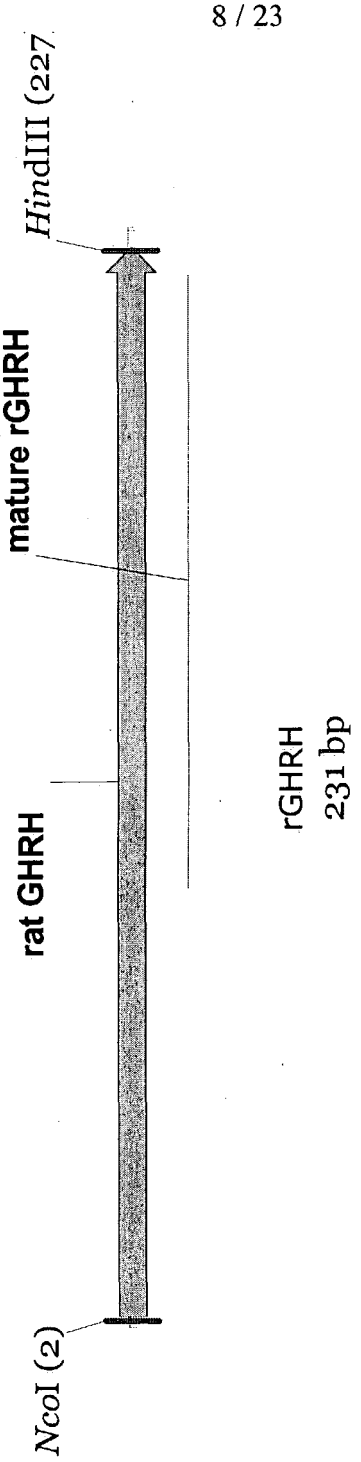
Figure 7



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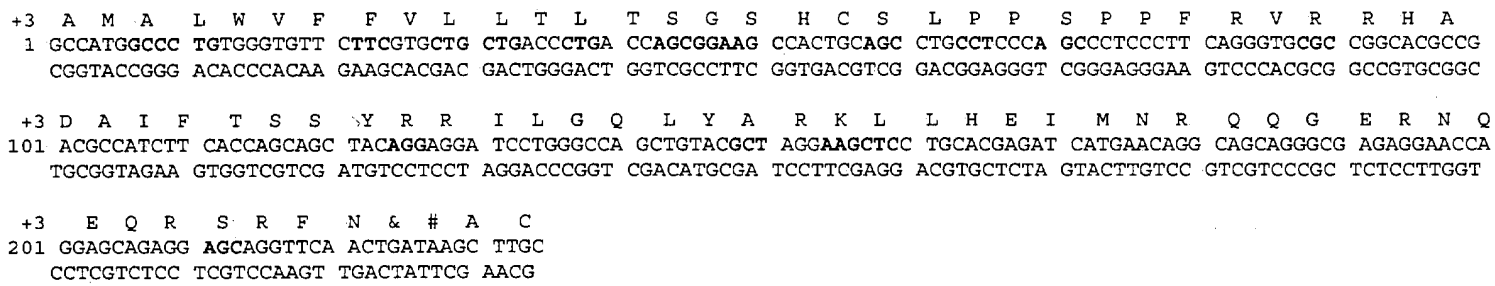
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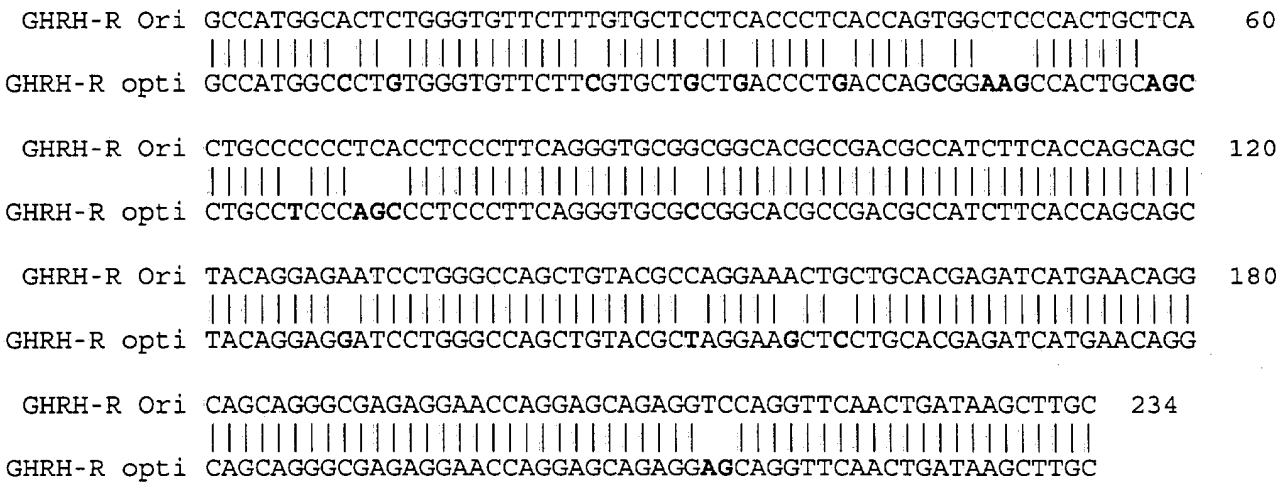
CGGTACCGGG ACACCCACAA GAAGCACGAC GACTGGGACT GGTCGCCTTC GGTGACGTCG GACGGAGGGT CGGGAGGGAA GTCCCACGCG GCCGTGCGGC
+3 D A I F T S S Y R R I L G Q L Y A R K L L H E I M N R Q Q G E R N Q
101 ACGCCATCTT CACCAGCAGC TACAGGAGGA TCCTGGGCCA GCTGTACGCT AGGAAGCTCC TGCACGAGAT CATGAACAGG CAGCAGGGCG AGAGGAACCA
TGCGGTAGAA GTGGTCGTCG ATGTCCTCCT AGGACCCGGT CGACATGCGA TCCTTCGAGG ACGTGCTCTA GTACTTGTCC GTCGTCCCGC TCTCCTTGGT
+3 E Q R S R F N & # A C
201 GGAGCAGAGG AGCAGGTTCA ACTGATAAGC TTGC
CCTCGTCTCC TCGTCCAAGT TGACTATTCG AACG

Figure 9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GHRH-R opti GCCATGGCCCTGTGGGTGTTCTTCGTGCTGCTGACCCTGACCAGCGGAAGCCACTGCAGC
GHRH-R Ori CTGCCCCCCTCACCTCCCTTCAGGGTGCGGCGGCACGCCGACGCCATCTTCACCAGCAGC 120
GHRH-R opti CTGCCTCCCAGCCCTCCCTTCAGGGTGCGCCGGCACGCCGACGCCATCTTCACCAGCAGC
GHRH-R Ori TACAGGAGAATCCTGGGCCAGCTGTACGCCAGGAAACTGCTGCACGAGATCATGAACAGG 180
GHRH-R opti TACAGGAGGATCCTGGGCCAGCTGTACGCTAGGAAGCTCCTGCACGAGATCATGAACAGG
GHRH-R Ori CAGCAGGGCGAGAGGAACCAGGAGCAGAGGTCCAGGTTCAACTGATAAGCTTGC 234
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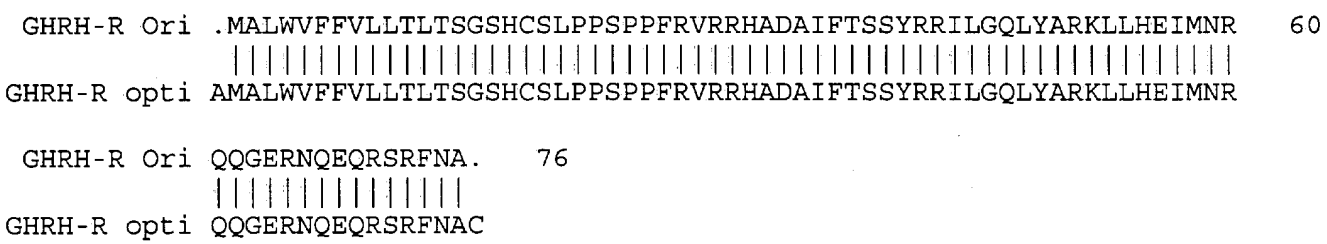
Figure 10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GHRH-R opti QQGERNQEQRSRFNAC

Figure 11

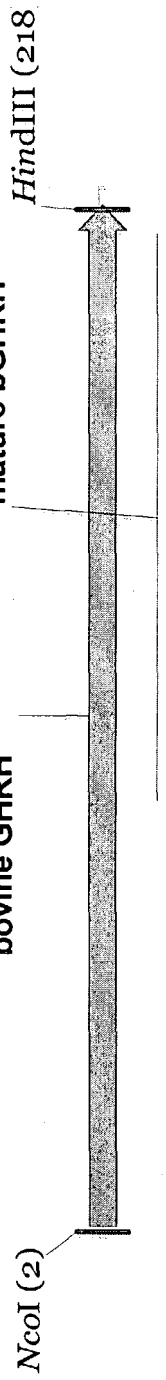

Figure 12


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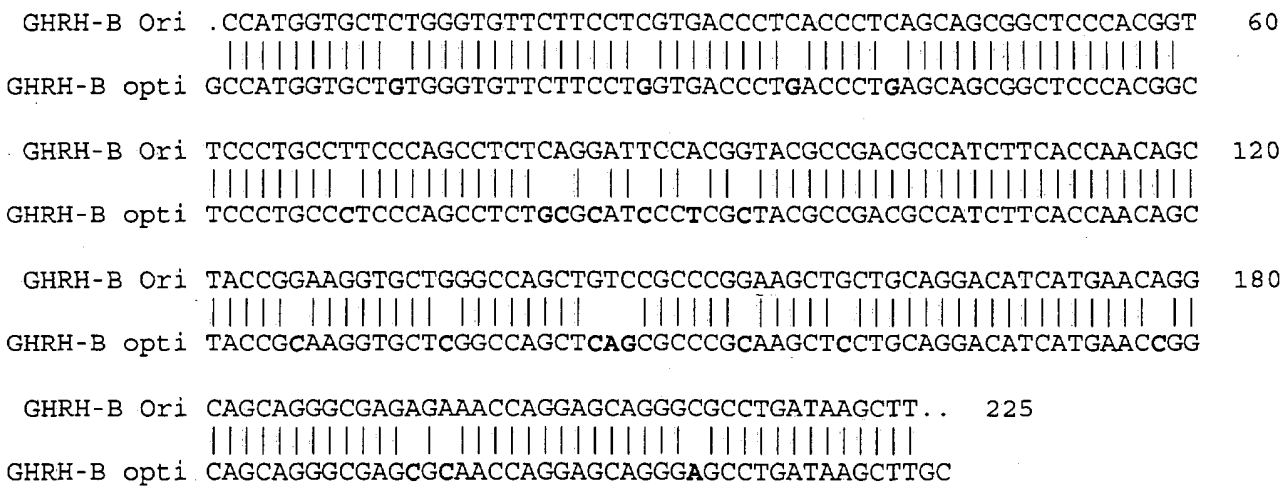
CGGTACCACG ACACCCACAA GAAGGACCAC TGGGACTGGG ACTCGTCGCC GAGGGTGCCG AGGGACGGGA GGGTCGGAGA CGCGTAGGGA GCGATGCGGC
+3 D A I F T N S Y R K V L G Q L S A R K L L Q D I M N R Q Q G E R N Q
101 ACGCCATCTT CACCAACAGC TACCGCAAGG TGCTCGGCCA GCTCAGCGCC CGCAAGCTCC TGCAGGACAT CATGAACCGG CAGCAGGGCG AGCGCAACCA
TGCGGTAGAA GTGGTTGTCG ATGGCGTTCC ACGAGCCGGT CGAGTCGCGG GCGTTCGAGG ACGTCCTGTA GTACTTGGCC GTCGTCCCGC TCGCGTTGGT
+3 E Q G A & # A C
201 GGAGCAGGGA GCCTGATAAG CTTGC
CCTCGTCCCT CGGACTATTC GAACG

Figure 13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GHRH-B opti GCCATGGTGCTGTGGGTGTTCTTCCTGGTGACCCTGACCCTGAGCAGCGGCTCCCACGGC
GHRH-B Ori TCCCTGCCTTCCCAGCCTCTCAGGATTCCACGGTACGCCGACGCCATCTTCACCAACAGC 120
GHRH-B opti TCCCTGCCCTCCCAGCCTCTGCGCATCCCTCGCTACGCCGACGCCATCTTCACCAACAGC
GHRH-B Ori TACCGGAAGGTGCTGGGCCAGCTGTCCGCCCGGAAGCTGCTGCAGGACATCATGAACAGG 180
GHRH-B opti TACCGCAAGGTGCTCGGCCAGCTCAGCGCCCGCAAGCTCCTGCAGGACATCATGAACCGG
GHRH-B Ori CAGCAGGGCGAGAGAAACCAGGAGCAGGGCGCCTGATAAGCTT.. 225
GHRH-B opti CAGCAGGGCGAGCGCAACCAGGAGCAGGGAGCCTGATAAGCTTGC

Figure 14

```
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GHRH-B opti AMVLWVFFLVTLTLSSGSHGSLPSQPLRIPRYADAIFTNSYRKVLGQLSARKLLQDIMNR

 GHRH-B Ori QQGERNQEQGAA.   73
            ||||||||||||
GHRH-B opti QQGERNQEQGAAC
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Figure 15

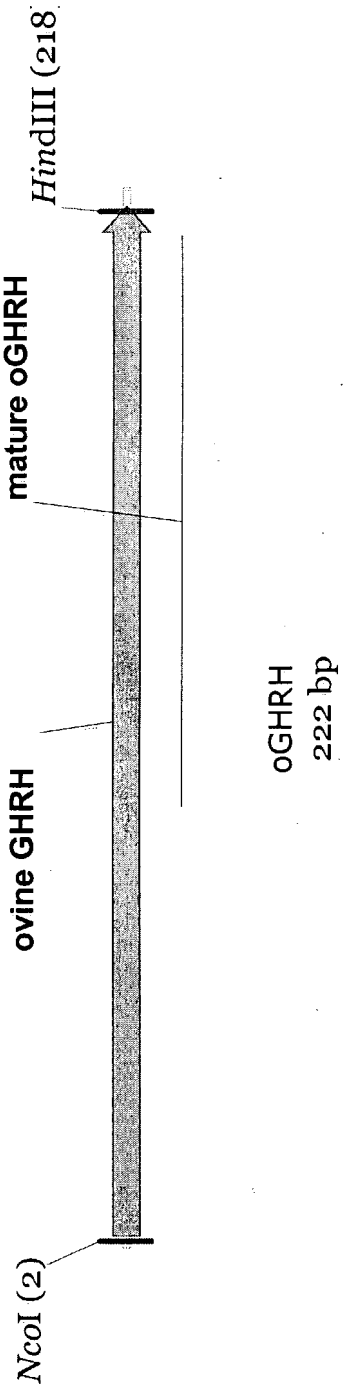
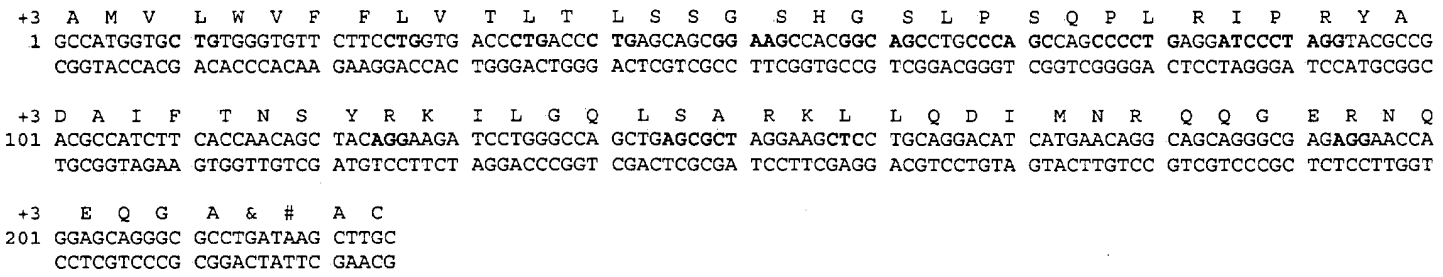


Figure 16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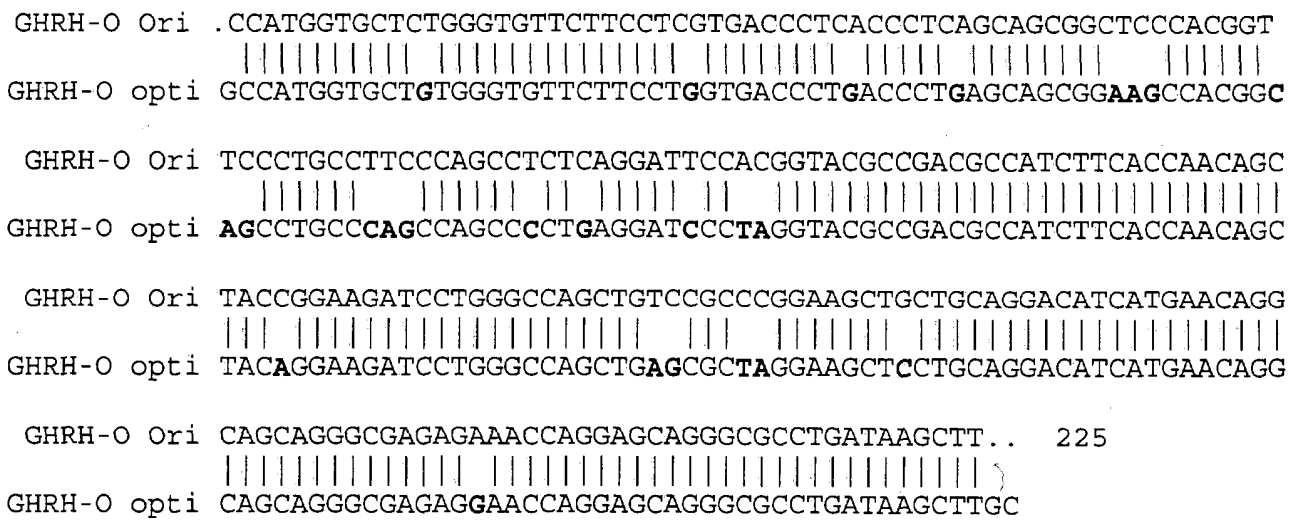
CGGTACCACG ACACCCACAA GAAGGACCAC TGGGACTGGG ACTCGTCGCC TTCGGTGCCG TCGGACGGGT CGGTCGGGGA CTCCTAGGGA TCCATGCGGC
+3 D A I F T N S Y R K I L G Q L S A R K L L Q D I M N R Q Q G E R N Q
101 ACGCCATCTT CACCAACAGC TACAGGAAGA TCCTGGGCCA GCTGAGCGCT AGGAAGCTCC TGCAGGACAT CATGAACAGG CAGCAGGGCG AGAGGAACCA
TGCGGTAGAA GTGGTTGTCG ATGTCCTTCT AGGACCCGGT CGACTCGCGA TCCTTCGAGG ACGTCCTGTA GTACTTGTCC GTCGTCCCGC TCTCCTTGGT
+3 E Q G A & # A C
201 GGAGCAGGGC GCCTGATAAG CTTGC
CCTCGTCCCG CGGACTATTC GAACG

Figure 17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GHRH-O Ori TCCCTGCCTTCCCAGCCTCTCAGGATTCCACGGTACGCCGACGCCATCTTCACCAACAGC 120
GHRH-O opti AGCCTGCCCAGCCAGCCCCTGAGGATCCCTAGGTACGCCGACGCCATCTTCACCAACAGC
GHRH-O Ori TACCGGAAGATCCTGGGCCAGCTGTCCGCCCGGAAGCTGCTGCAGGACATCATGAACAGG 180
GHRH-O opti TACAGGAAGATCCTGGGCCAGCTGAGCGCTAGGAAGCTCCTGCAGGACATCATGAACAGG
GHRH-O Ori CAGCAGGGCGAGAGAAACCAGGAGCAGGGCGCCTGATAAGCTT.. 225
GHRH-O opti CAGCAGGGCGAGAGGAACCAGGAGCAGGGCGCCTGATAAGCTTGC

Figure 18

```
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GHRH-O opti AMVLWVFFLVTLTLSSGSHGSLPSQPLRIPRYADAIFTNSYRKILGQLSARKLLQDIMNR

GHRH-O Ori  QQGERNQEQGAA.   73
            ||||||||||||
GHRH-O opti QQGERNQEQGAAC
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Figure 19

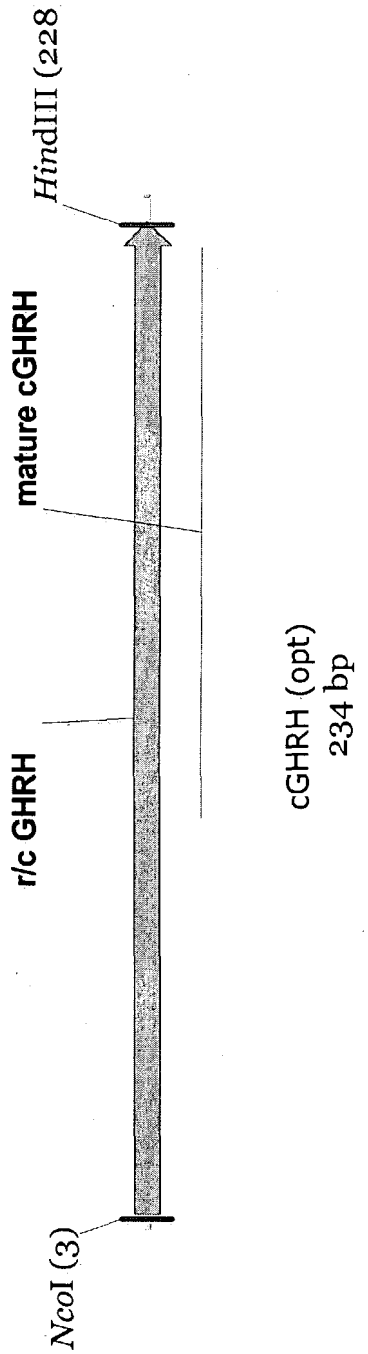
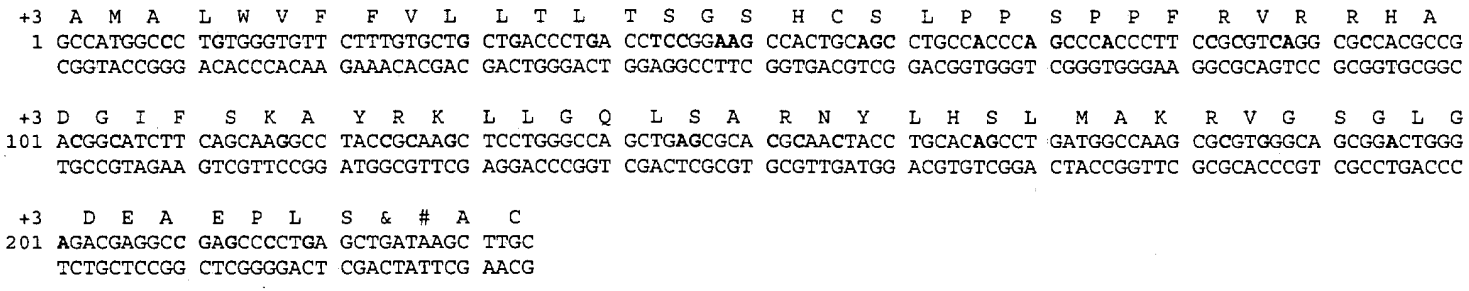


Figure 20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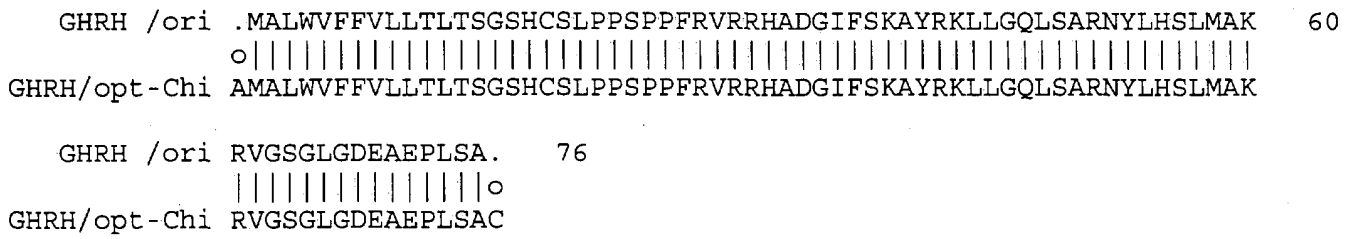
+3 D G I F S K A Y R K L L G Q L S A R N Y L H S L M A K R V G S G L G
101 ACGGCATCTT CAGCAAGGCC TACCGCAAGC TCCTGGGCCA GCTGAGCGCA CGCAACTACC TGCACAGCCT GATGGCCAAG CGCGTGGGCA GCGGACTGGG
TGCCGTAGAA GTCGTTCCGG ATGGCGTTCG AGGACCCGGT CGACTCGCGT GCGTTGATGG ACGTGTCGGA CTACCGGTTC GCGCACCCGT CGCCTGACCC
+3 D E A E P L S & # A C
201 AGACGAGGCC GAGCCCCTGA GCTGATAAGC TTGC
TCTGCTCCGG CTCGGGGACT CGACTATTCG AACG

Figure 21


GHRH /ori .CCATGGCACTCTGGGTGTTCTTTGTGCTCCTCACCCTCACCAGTGGCTCCCACTGCTCA 60
GHRH/opt-Chi GCCATGGCCCTGTGGGTGTTCTTTGTGCTGCTGACCCTGACCTCCGGAAGCCACTGCAGC
GHRH /ori CTGCCCCCCTCACCTCCCTTCAGGGTGCGGCGGCACGCCGATGGGATCTTCAGCAAAGCC 120
GHRH/opt-Chi CTGCCACCCAGCCCACCCTTCCGCGTCAGGCGCCACGCCGACGGCATCTTCAGCAAGGCC
GHRH /ori TACAGGAAACTCCTGGGCCAGCTGTCCGCAAGAAATTACCTGCACTCCCTGATGGCCAAG 180
GHRH/opt-Chi TACCGCAAGCTCCTGGGCCAGCTGAGCGCACGCAACTACCTGCACAGCCTGATGGCCAAG
GHRH /ori CGGGTCGGCAGCGGCCTGGGGGACGAGGCGGAACCGCTCAGCTGATAAGCTT.. 234
GHRH/opt-Chi CGCGTGGGCAGCGGACTGGGAGACGAGGCCGAGCCCCTGAGCTGATAAGCTTGC

Figure 22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GHRH/opt-Chi AMALWVFFVLLTLTSGSHCSLPPSPPFRVRRHADGIFSKAYRKLLGQLSARNYLHSLMAK
GHRH /ori RVGSGLGDEAEPLSA. 76
GHRH/opt-Chi RVGSGLGDEAEPLSAC

Figure 23